



US-108
SEQUENCE LISTING

<110> Ajinomoto Co., Inc.

<120> Inosine producing bacterium belonging to the genus
Bacillus and method for producing inosine

<130> US-108

<150> JP 2003-37760

<151> 2003-02-17

<160> 16

<170> PatentIn Ver. 2.0

<210> 1

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 1

ctcaagcttg aagttgcgat gatcaaaa

28

<210> 2

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 2

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28

<210> 3

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 3

ctcgtcgaca aaacgaatgg aagcgaacg

29

<210> 4

<211> 29

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: primer

<400> 4
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<210> 5
<211> 29
<212> DNA
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<220>
<223> Description of Artificial Sequence: primer

<400> 5
ctcgaattcc agcggaaatat tctttcccg 29

<210> 6
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<212> DNA
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ctcggatccc ggcaaaagca cagtatcc 28

<210> 7
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ctcaagctta tggtttccag accatcgact 30

<210> 8
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<223> Description of Artificial Sequence: primer

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ctcggatccc atgatatgtat agaagtgg 28

<210> 9
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<223> Description of Artificial Sequence: primer

<400> 9
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<210> 10
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<223> Description of Artificial Sequence: primer

<400> 10
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<210> 11
<211> 1200
<212> DNA
<213> *Bacillus subtilis*

<220>
<221> CDS
<222> (259)..(1113)

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agagaattta taacgggttta agaggcttct gcgatcaagt ttatgcgggtg agaatgatcg 180
gcgaacagaa cgctcttgcataaattccgtatgtttaatggta tattgtatctt aaaatattcg 240
gattttgggg gtgagttc atg aag ttt cgt cgc agc ggc aga ttg gtg gac 291
Met Lys Phe Arg Arg Ser Gly Arg Leu Val Asp
1 5 10
tta aca aat tat ttg tta acc cat ccg cac gag tta ata ccg cta acc 339
Leu Thr Asn Tyr Leu Leu Thr His Pro His Glu Leu Ile Pro Leu Thr
15 20 25
ttt ttc tct gag cgg tat gaa tct gca aaa tca tcg atc agt gaa gat 387
Phe Phe Ser Glu Arg Tyr Glu Ser Ala Lys Ser Ser Ile Ser Glu Asp
30 35 40
tta aca att att aaa caa acc ttt gaa cag cag ggg att ggt act ttg 435
Leu Thr Ile Ile Lys Gln Thr Phe Glu Gln Gln Gly Ile Gly Thr Leu
45 50 55
ctt act gtt ccc gga gct gcc gga ggc gtt aaa tat att ccg aaa atg 483
Leu Thr Val Pro Gly Ala Ala Gly Val Lys Tyr Ile Pro Lys Met
60 65 70 75
aag cag gct gaa gct gaa gag ttt gtg cag aca ctt gga cag tcg ctg 531
Lys Gln Ala Glu Ala Glu Glu Phe Val Gln Thr Leu Gly Gln Ser Leu
80 85 90
gca aat cct gag cgt atc ctt ccg ggc ggt tat gta tat tta acg gat 579
Ala Asn Pro Glu Arg Ile Leu Pro Gly Gly Tyr Val Tyr Leu Thr Asp
95 100 105
atc tta gga aag cca tct gta ctc tcc aag gta ggg aag ctg ttt gct 627
Ile Leu Gly Lys Pro Ser Val Leu Ser Lys Val Gly Lys Leu Phe Ala
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<210> 12

<211> 285

<212> PRT

<213> *Bacillus subtilis*

<400> 12

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      20          25          30
Tyr Glu Ser Ala Lys Ser Ser Ile Ser Glu Asp Leu Thr Ile Ile Lys
      35          40          45
Gln Thr Phe Glu Gln Gln Gly Ile Gly Thr Leu Leu Thr Val Pro Gly
      50          55          60
Ala Ala Gly Gly Val Lys Tyr Ile Pro Lys Met Lys Gln Ala Glu Ala
      65          70          75          80
Glu Glu Phe Val Gln Thr Leu Gly Gln Ser Leu Ala Asn Pro Glu Arg
      85          90          95
Ile Leu Pro Gly Gly Tyr Val Tyr Leu Thr Asp Ile Leu Gly Lys Pro
      100         105         110
Ser Val Leu Ser Lys Val Gly Lys Leu Phe Ala Ser Val Phe Ala Glu

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115						120					125				
130						135					140				
Ala	Tyr	Ala	Ala	Ala	Ser	Tyr	Leu	Asn	Val	Pro	Val	Val	Ile	Val	Arg
145						150					155				160
Lys	Asp	Asn	Lys	Val	Thr	Glu	Gly	Ser	Thr	Val	Ser	Ile	Asn	Tyr	Val
						165					170				175
Ser	Gly	Ser	Ser	Asn	Arg	Ile	Gln	Thr	Met	Ser	Leu	Ala	Lys	Arg	Ser
						180					185				190
Met	Lys	Thr	Gly	Ser	Asn	Val	Leu	Ile	Ile	Asp	Asp	Phe	Met	Lys	Ala
						195					200				205
Gly	Gly	Thr	Ile	Asn	Gly	Met	Ile	Asn	Leu	Leu	Asp	Glu	Phe	Asn	Ala
						210					215				220
Asn	Val	Ala	Gly	Ile	Gly	Val	Leu	Val	Glu	Ala	Glu	Gly	Val	Asp	Glu
						225					230				240
Arg	Leu	Val	Asp	Glu	Tyr	Met	Ser	Leu	Leu	Thr	Leu	Ser	Thr	Ile	Asn
						245					250				255
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Phe	Lys	Asp	Asn	Leu	Leu	Lys	Asn	Gly	Glu	Thr	Glu	Ser			
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<210> 13

<211> 1490

<212> DNA

<213> *Bacillus subtilis*

<220>

<221> CDS

<222> (101)..(1393)

<400> 13

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				Met	Ser	Ser	Val	Val									
				1			5										
gta	gta	ggt	acg	caa	tgg	gdc	gat	gaa	gga	aaa	ggt	aaa	att	aca	gat	163	
Val	Val	Gly	Thr	Gln	Trp	Gly	Asp	Glu	Gly	Lys	Gly	Lys	Ile	Thr	Asp		
				10			15						20				
ttc	cta	tca	gaa	aat	gca	gaa	gtg	atc	gcc	cgt	tat	caa	ggc	gga	aat	211	
Phe	Leu	Ser	Glu	Asn	Ala	Glu	Val	Ile	Ala	Arg	Tyr	Gln	Gly	Gly	Asn		
				25			30					35					
aac	gca	ggg	cat	aca	atc	aag	ttt	gac	gga	atc	aca	tat	aag	ctt	cac	259	
Asn	Ala	Gly	His	Thr	Ile	Lys	Phe	Asp	Gly	Ile	Thr	Tyr	Lys	Leu	His		
				40			45					50					
tta	atc	ccg	tct	gga	att	ttc	tat	aag	gat	aaa	acg	tgt	gta	atc	gga	307	
Leu	Ile	Pro	Ser	Gly	Ile	Phe	Tyr	Lys	Asp	Lys	Thr	Cys	Val	Ile	Gly		
				55			60					65					
aac	gga	atg	gtt	gta	gat	ccg	aaa	gca	tta	gtc	aca	gag	ctt	gcg	tat	355	
Asn	Gly	Met	Val	Val	Asp	Pro	Lys	Ala	Leu	Val	Thr	Glu	Leu	Ala	Tyr		
				70			75					80			85		
ctt	cat	gag	cgc	aac	gtg	agt	aca	gat	aac	ctg	aga	atc	agc	aac	aga	403	
Leu	His	Glu	Arg	Asn	Val	Ser	Thr	Asp	Asn	Leu	Arg	Ile	Ser	Asn	Arg		
				90			95					100					
gct	cac	gtc	att	ctg	ccg	tat	cat	ttg	aaa	ttg	gat	gaa	gtg	gaa	gaa	451	

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Ala	His	Val	Ile	Leu	Pro	Tyr	His	Leu	Lys	Leu	Asp	Glu	Val	Glu	Glu	
105				110							115					
gag	cgt	aaa	ggg	gct	aac	aag	atc	ggc	aca	acg	aaa	aaa	gga	atc	gac	499
Glu	Arg	Lys	Gly	Ala	Asn	Lys	Ile	Gly	Thr	Thr	Lys	Lys	Gly	Ile	Gly	
120				125							130					
cct	gct	tac	atg	gat	aaa	gca	gcc	cgc	atc	gga	att	cgc	atc	gac	gat	547
Pro	Ala	Tyr	Met	Asp	Lys	Ala	Ala	Arg	Ile	Gly	Ile	Arg	Ile	Ala	Asp	
135			140								145					
ctg	tta	gac	cgt	gac	gcg	ttt	gct	gaa	aag	ctt	gag	cgc	aat	ctt	gaa	595
Leu	Leu	Asp	Arg	Asp	Ala	Phe	Ala	Glu	Lys	Leu	Glu	Arg	Asn	Leu	Glu	
150			155							160					165	
gaa	aaa	aac	cgt	ctt	ctc	gag	aaa	atg	tac	gag	aca	gaa	ggg	ttt	aaa	643
Glu	Lys	Asn	Arg	Leu	Leu	Glu	Lys	Met	Tyr	Glu	Thr	Glu	Gly	Phe	Lys	
170									175					180		
ctt	gag	gat	atc	tta	gac	gaa	tat	tat	gag	tac	gga	cag	cag	att	aaa	691
Leu	Glu	Asp	Ile	Leu	Asp	Glu	Tyr	Tyr	Glu	Tyr	Gly	Gln	Gln	Ile	Lys	
185									190				195			
aag	tat	gtt	tgc	gat	aca	tct	gtt	gtc	tta	aac	gat	gct	ctt	gat	gaa	739
Lys	Tyr	Val	Cys	Asp	Thr	Ser	Val	Val	Leu	Asn	Asp	Ala	Leu	Asp	Glu	
200									205				210			
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Gly	Arg	Arg	Val	Leu	Phe	Glu	Gly	Ala	Gln	Gly	Val	Met	Leu	Asp	Ile	
215					220					225						
gac	caa	gga	aca	tac	ccg	ttt	gtt	acg	tca	tct	aac	ccg	gtt	gcc	ggc	835
Asp	Gln	Gly	Thr	Tyr	Pro	Phe	Val	Thr	Ser	Ser	Asn	Pro	Val	Ala	Gly	
230					235					240				245		
ggt	gtc	acg	atc	ggt	tct	ggt	gtc	ggc	ccg	acc	aaa	atc	aag	cac	gtt	883
Gly	Val	Thr	Ile	Gly	Ser	Gly	Val	Gly	Pro	Thr	Lys	Ile	Lys	His	Val	
250									255				260			
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Val	Gly	Val	Ser	Lys	Ala	Tyr	Thr	Thr	Arg	Val	Gly	Asp	Gly	Pro	Phe	
265									270				275			
ccg	act	gag	ctg	aaa	gat	gaa	atc	ggc	gat	caa	atc	cgt	gaa	gtc	gga	979
Pro	Thr	Glu	Leu	Lys	Asp	Glu	Ile	Gly	Asp	Gln	Ile	Arg	Glu	Val	Gly	
280									285				290			
cgc	gaa	tat	gga	aca	aca	aca	ggc	cgc	ccg	cgc	cgt	gtc	ggc	tgg	ttt	1027
Arg	Glu	Tyr	Gly	Thr	Thr	Thr	Gly	Arg	Pro	Arg	Arg	Val	Gly	Trp	Phe	
295					300					305						
gac	agc	gtt	gtt	gtc	cgc	cac	gcc	cgc	cgt	gtg	agc	gga	att	aca	gat	1075
Asp	Ser	Val	Val	Val	Arg	His	Ala	Arg	Arg	Val	Ser	Gly	Ile	Thr	Asp	
310									315			320			325	
ctt	tct	ctg	aac	tca	att	gac	gtc	cta	gca	gga	att	gaa	acg	ttg	aaa	1123
Leu	Ser	Leu	Asn	Ser	Ile	Asp	Val	Leu	Ala	Gly	Ile	Glu	Thr	Leu	Lys	
330									335			340				
atc	tgt	gtg	gct	tac	cgc	tac	aaa	ggc	gaa	atc	att	gaa	gaa	ttc	cca	1171
Ile	Cys	Val	Ala	Tyr	Arg	Tyr	Lys	Gly	Glu	Ile	Ile	Glu	Glu	Phe	Pro	
345								350				355				
gca	agt	ctt	aag	gca	ctt	gct	gaa	tgt	gag	ccg	gta	tat	gaa	gaa	atg	1219
Ala	Ser	Leu	Lys	Ala	Leu	Ala	Glu	Cys	Glu	Pro	Val	Tyr	Glu	Glu	Met	
360								365			370					
ccg	ggc	tgg	act	gag	gat	att	aca	ggt	gct	aag	agc	ttg	agc	gag	ctt	1267
Pro	Gly	Trp	Thr	Glu	Asp	Ile	Thr	Gly	Ala	Lys	Ser	Leu	Ser	Glu	Leu	
375								380			385					
ccg	gaa	aat	gct	cgc	cat	tat	ctt	gag	cgt	gtg	tct	cag	ctg	aca	ggc	1315
Pro	Glu	Asn	Ala	Arg	His	Tyr	Leu	Glu	Arg	Val	Ser	Gln	Leu	Thr	Gly	

	390	395	400	405	
	att ccg ctt tct att ttc tct gtc ggt cca gac cgc tca caa aca aat				
Ile Pro Leu Ser Ile Phe Ser Val Gly Pro Asp Arg Ser Gln Thr Asn					1363
410		415		420	
gtc ctt cgc agt gtg tac cgt gcg aac taa atagaatatg tctgcaagcc					1413
Val Leu Arg Ser Val Tyr Arg Ala Asn					
425		430			
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<210> 14

<211> 430

<212> PRT

<213> *Bacillus subtilis*

<400> 14

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Tyr Gln Gly Asn Asn Ala Gly His Thr Ile Lys Phe Asp Gly Ile		35	40	45		
Thr Tyr Lys Leu His Leu Ile Pro Ser Gly Ile Phe Tyr Lys Asp Lys		50	55	60		
Thr Cys Val Ile Gly Asn Gly Met Val Val Asp Pro Lys Ala Leu Val		65	70	75	80	
Thr Glu Leu Ala Tyr Leu His Glu Arg Asn Val Ser Thr Asp Asn Leu		85	90	95		
Arg Ile Ser Asn Arg Ala His Val Ile Leu Pro Tyr His Leu Lys Leu		100	105	110		
Asp Glu Val Glu Glu Glu Arg Lys Gly Ala Asn Lys Ile Gly Thr Thr		115	120	125		
Lys Lys Gly Ile Gly Pro Ala Tyr Met Asp Lys Ala Ala Arg Ile Gly		130	135	140		
Ile Arg Ile Ala Asp Leu Leu Asp Arg Asp Ala Phe Ala Glu Lys Leu		145	150	155	160	
Glu Arg Asn Leu Glu Glu Lys Asn Arg Leu Leu Glu Lys Met Tyr Glu		165	170	175		
Thr Glu Gly Phe Lys Leu Glu Asp Ile Leu Asp Glu Tyr Tyr Glu Tyr		180	185	190		
Gly Gln Gln Ile Lys Lys Tyr Val Cys Asp Thr Ser Val Val Leu Asn		195	200	205		
Asp Ala Leu Asp Glu Gly Arg Arg Val Leu Phe Glu Gly Ala Gln Gly		210	215	220		
Val Met Leu Asp Ile Asp Gln Gly Thr Tyr Pro Phe Val Thr Ser Ser		225	230	235	240	
Asn Pro Val Ala Gly Gly Val Thr Ile Gly Ser Gly Val Gly Pro Thr		245	250	255		
Lys Ile Lys His Val Val Gly Val Ser Lys Ala Tyr Thr Thr Arg Val		260	265	270		
Gly Asp Gly Pro Phe Pro Thr Glu Leu Lys Asp Glu Ile Gly Asp Gln		275	280	285		
Ile Arg Glu Val Gly Arg Glu Tyr Gly Thr Thr Thr Gly Arg Pro Arg		290	295	300		
Arg Val Gly Trp Phe Asp Ser Val Val Val Arg His Ala Arg Arg Val						

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305	310	315	320												
Ser	Gly	Ile	Thr	Asp	Leu	Ser	Leu	Asn	Ser	Ile	Asp	Val	Leu	Ala	Gly
325	330	335													
Ile	Glu	Thr	Leu	Lys	Ile	Cys	Val	Ala	Tyr	Arg	Tyr	Lys	Gly	Glu	Ile
340	345	350													
Ile	Glu	Glu	Phe	Pro	Ala	Ser	Leu	Lys	Ala	Leu	Ala	Glu	Cys	Glu	Pro
355	360	365													
Val	Tyr	Glu	Glu	Met	Pro	Gly	Trp	Thr	Glu	Asp	Ile	Thr	Gly	Ala	Lys
370	375	380													
Ser	Leu	Ser	Glu	Leu	Pro	Glu	Asn	Ala	Arg	His	Tyr	Leu	Glu	Arg	Val
385	390	395	400												
Ser	Gln	Leu	Thr	Gly	Ile	Pro	Leu	Ser	Ile	Phe	Ser	Val	Gly	Pro	Asp
405	410	415													
Arg	Ser	Gln	Thr	Asn	Val	Leu	Arg	Ser	Val	Tyr	Arg	Ala	Asn		
420	425	430													

<210> 15

<211> 899

<212> DNA

<213> *Bacillus subtilis*

<220>

<221> CDS

<222> (101)..(802)

<400> 15

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				Met	Ser	Val	His	Ile								
				1			5									
ggt	gct	aaa	gga	caa	att	gcg	gat	act	gtg	ctt	ttg	ccg	gga	gat	163	
Gly	Ala	Glu	Lys	Gly	Gln	Ile	Ala	Asp	Thr	Val	Leu	Leu	Pro	Gly	Asp	
10						15			20							
cct	ctc	aga	gca	aaa	ttt	att	gca	gaa	acg	tat	ctt	gaa	aat	gta	gaa	211
Pro	Leu	Arg	Ala	Lys	Phe	Ile	Ala	Glu	Thr	Tyr	Leu	Glu	Asn	Val	Glu	
25						30			35							
tgc	tac	aat	gaa	gtc	aga	ggc	atg	tat	gga	ttt	acg	ggt	aca	tat	aaa	259
Cys	Tyr	Asn	Glu	Val	Arg	Gly	Met	Tyr	Gly	Phe	Thr	Gly	Thr	Tyr	Lys	
40						45			50							
ggt	aaa	aaa	atc	tca	gta	caa	ggc	acg	gga	atg	gga	gtt	ccg	tct	att	307
Gly	Lys	Lys	Ile	Ser	Val	Gln	Gly	Thr	Gly	Met	Gly	Val	Pro	Ser	Ile	
55						60			65							
tca	att	tat	gtg	aat	gaa	tta	att	caa	agc	tac	gat	gtg	caa	aat	cta	355
Ser	Ile	Tyr	Val	Asn	Glu	Leu	Ile	Gln	Ser	Tyr	Asp	Val	Gln	Asn	Leu	
70						75			80			85				
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Ile	Arg	Val	Gly	Ser	Cys	Gly	Ala	Ile	Arg	Lys	Asp	Val	Lys	Val	Arg	
90						95			100							
gac	gtc	att	ttg	gcg	atg	acc	tcc	tca	act	gat	tca	caa	atg	aac	aga	451
Asp	Val	Ile	Leu	Ala	Met	Thr	Ser	Ser	Thr	Asp	Ser	Gln	Met	Asn	Arg	
105						110			115							
gtt	gct	ttc	gga	agc	gtt	gat	ttt	gcg	cct	tgc	gca	gat	ttc	gag	ctt	499
Val	Ala	Phe	Gly	Ser	Val	Asp	Phe	Ala	Pro	Cys	Ala	Asp	Phe	Glu	Leu	
120						125			130							
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<210> 16
<211> 233
<212> PRT
<213> *Bacillus subtilis*

<400> 16
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 35 40 45
 Thr Gly Thr Tyr Lys Gly Lys Ile Ser Val Gln Gly Thr Gly Met
 50 55 60
 Gly Val Pro Ser Ile Ser Ile Tyr Val Asn Glu Leu Ile Gln Ser Tyr
 65 70 75 80
 Asp Val Gln Asn Leu Ile Arg Val Gly Ser Cys Gly Ala Ile Arg Lys
 85 90 95
 Asp Val Lys Val Arg Asp Val Ile Leu Ala Met Thr Ser Ser Thr Asp
 100 105 110
 Ser Gln Met Asn Arg Val Ala Phe Gly Ser Val Asp Phe Ala Pro Cys
 115 120 125
 Ala Asp Phe Glu Leu Leu Lys Asn Ala Tyr Asp Ala Ala Lys Asp Lys
 130 135 140
 Gly Val Pro Val Thr Val Gly Ser Val Phe Thr Ala Asp Gln Phe Tyr
 145 150 155 160
 Asn Asp Asp Ser Gln Ile Glu Lys Leu Ala Lys Tyr Gly Val Leu Gly
 165 170 175
 Val Glu Met Glu Thr Thr Ala Leu Tyr Thr Leu Ala Ala Lys His Gly
 180 185 190
 Arg Lys Ala Leu Ser Ile Leu Thr Val Ser Asp His Val Leu Thr Gly
 195 200 205
 Glu Glu Thr Thr Ala Glu Glu Arg Gln Thr Thr Phe His Asp Met Ile

210 Glu Val Ala Leu His Ser Val Ser Gln
215 220
225 230

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